

V. PORTNER

1645

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/284,233A  
DATE: 01/08/2001  
TIME: 14:59:51

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5 <110> APPLICANT: Meyer, Thomas  
7 Haas, Rainer  
9 Zhengxin, Yan  
11 Gomez-Duarte, Oscar  
13 Lucas, Bernadette  
17 <120> TITLE OF INVENTION: Helicobacter pylori live vaccine  
21 <130> FILE REFERENCE: 100564-09008  
25 <140> CURRENT APPLICATION NUMBER: 09/284,233A  
27 <141> CURRENT FILING DATE: 1999-07-28  
31 <150> PRIOR APPLICATION NUMBER: PCT/EP97/04744  
33 <151> PRIOR FILING DATE: 1997-09-01  
37 <150> PRIOR APPLICATION NUMBER: EP/96 116 337.5  
39 <151> PRIOR FILING DATE: 1996-10-11  
43 <160> NUMBER OF SEQ ID NOS: 9  
47 <170> SOFTWARE: PatentIn version 3.0  
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55 <212> TYPE: DNA  
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65 <222> LOCATION: (1)..(1554)  
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72 1 5 10 15  
74 tta agc ttg agc ttc aat cca gtg ggc gct gaa gaa gat ggg ggc ttt 96  
75 Leu Ser Leu Ser Phe Asn Pro Val Gly Ala Glu Glu Asp Gly Gly Phe  
76 20 25 30  
78 atg acc ttt ggg tat gaa tta ggt cag gtg gtc caa caa gtg aaa aac 144  
79 Met Thr Phe Gly Tyr Glu Leu Gly Gln Val Val Gln Gln Val Lys Asn  
80 35 40 45  
82 ccg ggt aaa atc aaa gcc gaa gaa tta gcc ggc ttg tta aac tct acc 192  
83 Pro Gly Lys Ile Lys Ala Glu Glu Leu Ala Gly Leu Leu Asn Ser Thr  
84 50 55 60  
86 aca aca aac aac acc aat atc aat att gca ggc aca gga ggc aat gtc 240  
87 Thr Thr Asn Asn Thr Asn Ile Asn Ile Ala Gly Thr Gly Gly Asn Val  
88 65 70 75 80  
90 gcc ggg act ttg ggc aac ctt ttt atg aac caa tta ggc aat ttg att 288  
91 Ala Gly Thr Leu Gly Asn Leu Phe Met Asn Gln Leu Gly Asn Leu Ile  
92 85 90 95  
94 gat ttg tat ccc act ttg aac act agt aat atc aca caa tgt ggc act 336  
95 Asp Leu Tyr Pro Thr Leu Asn Thr Ser Asn Ile Thr Gln Cys Gly Thr  
96 100 105 110  
98 act aat agt ggt agt agt agt agt ggt ggt ggc gcc aca gcc gct 384  
99 Thr Asn Ser Gly Ser Ser Ser Ser Gly Gly Gly Ala Ala Thr Ala Ala  
100 115 120 125

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103	Ala Thr Thr Ser Asn Lys Pro Cys Phe Gln Gly Asn Leu Asp Leu Tyr	
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106	aga aaa atg gtt gac tct atc aaa act ttg agt caa aac atc agc aag	480
107	Arg Lys Met Val Asp Ser Ile Lys Thr Leu Ser Gln Asn Ile Ser Lys	
108	145 150 155 160	
110	aat atc ttt caa ggc aac aac aac acc acg agc caa aat ctc tcc aac	528
111	Asn Ile Phe Gln Gly Asn Asn Asn Thr Thr Ser Gln Asn Leu Ser Asn	
112	165 170 175	
114	cag ctc agt gag ctt aac acc gct agc gtt tat ttg act tac atg aac	576
115	Gln Leu Ser Glu Leu Asn Thr Ala Ser Val Tyr Leu Thr Tyr Met Asn	
116	180 185 190	
118	tcg ttc tta aac gcc aat aac caa gcg ggt ggg att ttt caa aac aac	624
119	Ser Phe Leu Asn Ala Asn Asn Gln Ala Gly Gly Ile Phe Gln Asn Asn	
120	195 200 205	
122	act aat caa gct tat gga aat ggg gtt acc gct caa caa atc gct tat	672
123	Thr Asn Gln Ala Tyr Gly Asn Gly Val Thr Ala Gln Gln Ile Ala Tyr	
124	210 215 220	
126	atc cta aag caa gct tca atc act atg ggg cca agc ggt gat agc ggt	720
127	Ile Leu Lys Gln Ala Ser Ile Thr Met Gly Pro Ser Gly Asp Ser Gly	
128	225 230 235 240	
130	gct gcc gca gcg ttt ttg gat gcc gct tta gcg caa cat gtt ttc aac	768
131	Ala Ala Ala Ala Phe Leu Asp Ala Ala Leu Ala Gln His Val Phe Asn	
132	245 250 255	
134	tcc gct aac gcc gcg aac gat ttg agc gct aag gaa ttc act agc ttg	816
135	Ser Ala Asn Ala Gly Asn Asp Leu Ser Ala Lys Glu Phe Thr Ser Leu	
136	260 265 270	
138	gtg caa aat atc gtc aat aat tct caa aac gct tta acg cta gcc aac	864
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140	275 280 285	
142	aac gct aac atc agc aat tca aca gcc tat caa gtg agc tat gcc ggg	912
143	Asn Ala Asn Ile Ser Asn Ser Thr Gly Tyr Gln Val Ser Tyr Gly Gly	
144	290 295 300	
146	aat att gat caa gcg cga tct acc caa cta tta aac aac acc aca aac	960
147	Asn Ile Asp Gln Ala Arg Ser Thr Gln Leu Leu Asn Asn Thr Thr Asn	
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150	act ttg gct aaa gtt agc gct ttg aat aac gag ctt aaa gct aac cca	1008
151	Thr Leu Ala Lys Val Ser Ala Leu Asn Asn Glu Leu Lys Ala Asn Pro	
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154	tggt ctt ggg aat ttt gcc gcc ggt aac agc tct caa gtg aat gcg ttt	1056
155	Trp Leu Gly Asn Phe Ala Ala Gly Asn Ser Ser Gln Val Asn Ala Phe	
156	340 345 350	
158	aac ggg ttt atc act aaa atc ggt tac aag caa ttc ttt ggg gaa aac	1104
159	Asn Gly Phe Ile Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Glu Asn	
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162	aag aat gtg ggc tta cgc tac tac ggc ttc ttc agc tat aac ggc gcg	1152
163	Lys Asn Val Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala	
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171 Gly Val Gly Thr Asp Val Leu Tyr Asn Val Phe Ser Arg Ser Phe Gly
172 405 410 415
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175 Ser Arg Ser Leu Asn Ala Gly Phe Phe Gly Gly Ile Gln Leu Ala Gly
176 420 425 430
178 gat act tac atc agc acg cta aga aac agc tct cag ctt gcg agc aga 1344
179 Asp Thr Tyr Ile Ser Thr Leu Arg Asn Ser Ser Gln Leu Ala Ser Arg
180 435 440 445
182 cct aca gcg acg aaa ttc caa ttc ttg ttt gat gtg ggc tta cgc atg 1392
183 Pro Thr Ala Thr Lys Phe Gln Phe Leu Phe Asp Val Gly Leu Arg Met
184 450 455 460
186 aac ttt ggt atc ttg aaa aaa gac ttg aaa agc cat aac cag cat tct 1440
187 Asn Phe Gly Ile Leu Lys Lys Asp Leu Lys Ser His Asn Gln His Ser
188 465 470 475 480
190 ata gaa atc ggt gtg caa atc cct acg att tac aac act tac tat aaa 1488
191 Ile Glu Ile Gly Val Gln Ile Pro Thr Ile Tyr Asn Thr Tyr Tyr Lys
192 485 490 495
194 gct ggc ggt gct gaa gtg aaa tac ttc cgc cct tat agc gtg tat tgg 1536
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224 35 40 45
227 Pro Gly Lys Ile Lys Ala Glu Glu Leu Ala Gly Leu Leu Asn Ser Thr
228 50 55 60
231 Thr Thr Asn Asn Thr Asn Ile Asn Ile Ala Gly Thr Gly Gly Asn Val
232 65 70 75 80
235 Ala Gly Thr Leu Gly Asn Leu Phe Met Asn Gln Leu Gly Asn Leu Ile
236 85 90 95
239 Asp Leu Tyr Pro Thr Leu Asn Thr Ser Asn Ile Thr Gln Cys Gly Thr
240 100 105 110
243 Thr Asn Ser Gly Ser Ser Ser Ser Gly Gly Gly Ala Ala Thr Ala Ala
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247 Ala Thr Thr Ser Asn Lys Pro Cys Phe Gln Gly Asn Leu Asp Leu Tyr
248 130 135 140

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259 Gln Leu Ser Glu Leu Asn Thr Ala Ser Val Tyr Leu Thr Tyr Met Asn
260 180 185 190
263 Ser Phe Leu Asn Ala Asn Asn Gln Ala Gly Gly Ile Phe Gln Asn Asn
264 195 200 205
267 Thr Asn Gln Ala Tyr Gly Asn Gly Val Thr Ala Gln Gln Ile Ala Tyr
268 210 215 220
271 Ile Leu Lys Gln Ala Ser Ile Thr Met Gly Pro Ser Gly Asp Ser Gly
272 225 230 235 240
275 Ala Ala Ala Ala Phe Leu Asp Ala Ala Leu Ala Gln His Val Phe Asn
276 245 250 255
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280 260 265 270
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284 275 280 285
287 Asn Ala Asn Ile Ser Asn Ser Thr Gly Tyr Gln Val Ser Tyr Gly Gly
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296 325 330 335
299 Trp Leu Gly Asn Phe Ala Ala Gly Asn Ser Ser Gln Val Asn Ala Phe
300 340 345 350
303 Asn Gly Phe Ile Thr Lys Ile Gly Tyr Lys Gln Phe Phe Gly Glu Asn
304 355 360 365
307 Lys Asn Val Gly Leu Arg Tyr Tyr Gly Phe Phe Ser Tyr Asn Gly Ala
308 370 375 380
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323 Asp Thr Tyr Ile Ser Thr Leu Arg Asn Ser Ser Gln Leu Ala Ser Arg
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327 Pro Thr Ala Thr Lys Phe Gln Phe Leu Phe Asp Val Gly Leu Arg Met
328 450 455 460
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351 <212> TYPE: DNA
353 <213> ORGANISM: Helicobacter pylori
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359 <221> NAME/KEY: CDS
361 <222> LOCATION: (1)..(1554)
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371 Ser Ile Ser Tyr Ala Glu Asp Asp Gly Gly Phe Phe Thr Val Gly Tyr
372 20 25 30
374 cag ctg ggg caa gtc atg caa gat gtc caa aac cca ggc ggc gct aaa      144
375 Gln Leu Gly Gln Val Met Gln Asp Val Gln Asn Pro Gly Gly Ala Lys
376 35 40 45
378 agc gac gaa ctg gcc aga gag ctt aac gct gat gta acg aac aac att      192
379 Ser Asp Glu Leu Ala Arg Glu Leu Asn Ala Asp Val Thr Asn Asn Ile
380 50 55 60
382 tta aac aac aac acc gga ggc aac atc gca ggg gcg ttg agt aac gct      240
383 Leu Asn Asn Asn Thr Gly Gly Asn Ile Ala Gly Ala Leu Ser Asn Ala
384 65 70 75 80
386 ttc tcc caa tac ctt tat tcg ctt tta ggg gct tac ccc aca aaa ctg      288
387 Phe Ser Gln Tyr Leu Tyr Ser Leu Leu Gly Ala Tyr Pro Thr Lys Leu
388 85 90 95
390 aat ggt agc gat gtg tct gcg aac gct ctt tta agt ggt gcg gta ggc      336
391 Asn Gly Ser Asp Val Ser Ala Asn Ala Leu Leu Ser Gly Ala Val Gly
392 100 105 110
394 tct ggg act tgt gcg gct gca ggg acg gct ggt ggc act tct ctt aac      384
395 Ser Gly Thr Cys Ala Ala Ala Gly Thr Ala Gly Gly Thr Ser Leu Asn
396 115 120 125
398 act caa agc act tgc acc gtt gcg ggc tat tac tgg ctg cct agc ttg      432
399 Thr Gln Ser Thr Cys Thr Val Ala Gly Tyr Tyr Trp Leu Pro Ser Leu
400 130 135 140
402 act gac agg att tta agc acg atc ggc agc cag act aac tac ggc acg      480
403 Thr Asp Arg Ile Leu Ser Thr Ile Gly Ser Gln Thr Asn Tyr Gly Thr
404 145 150 155 160
406 aac acc aat ttc ccc aac atg caa caa cag ctg acc tac ttg aat gcg      528
407 Asn Thr Asn Phe Pro Asn Met Gln Gln Gln Leu Thr Tyr Leu Asn Ala
408 165 170 175
410 ggg aat gtg ttt ttt aat gcg atg aat aag gct tta gag aat aag aat      576
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412 180 185 190
414 gga act agt agt gct agt gga act agt ggt gcg act ggt tca gat ggt      624
415 Gly Thr Ser Ser Ala Ser Gly Thr Ser Gly Ala Thr Gly Ser Asp Gly
416 195 200 205
418 caa act tac tcc aca caa gct atc caa tac ctt caa ggc caa caa aat      672
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VERIFICATION SUMMARY

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